

DOTF80" 4254E960

Tubes Cluster Patterns: C0H C6H C1D C2D C4D C6D
 N Cls: 4 - P ANDVA: 0.0005 - Tubes Present: PNull < 0.0005 and Min FC: 2.5
 Hu Map Present: PNull < 0.000005

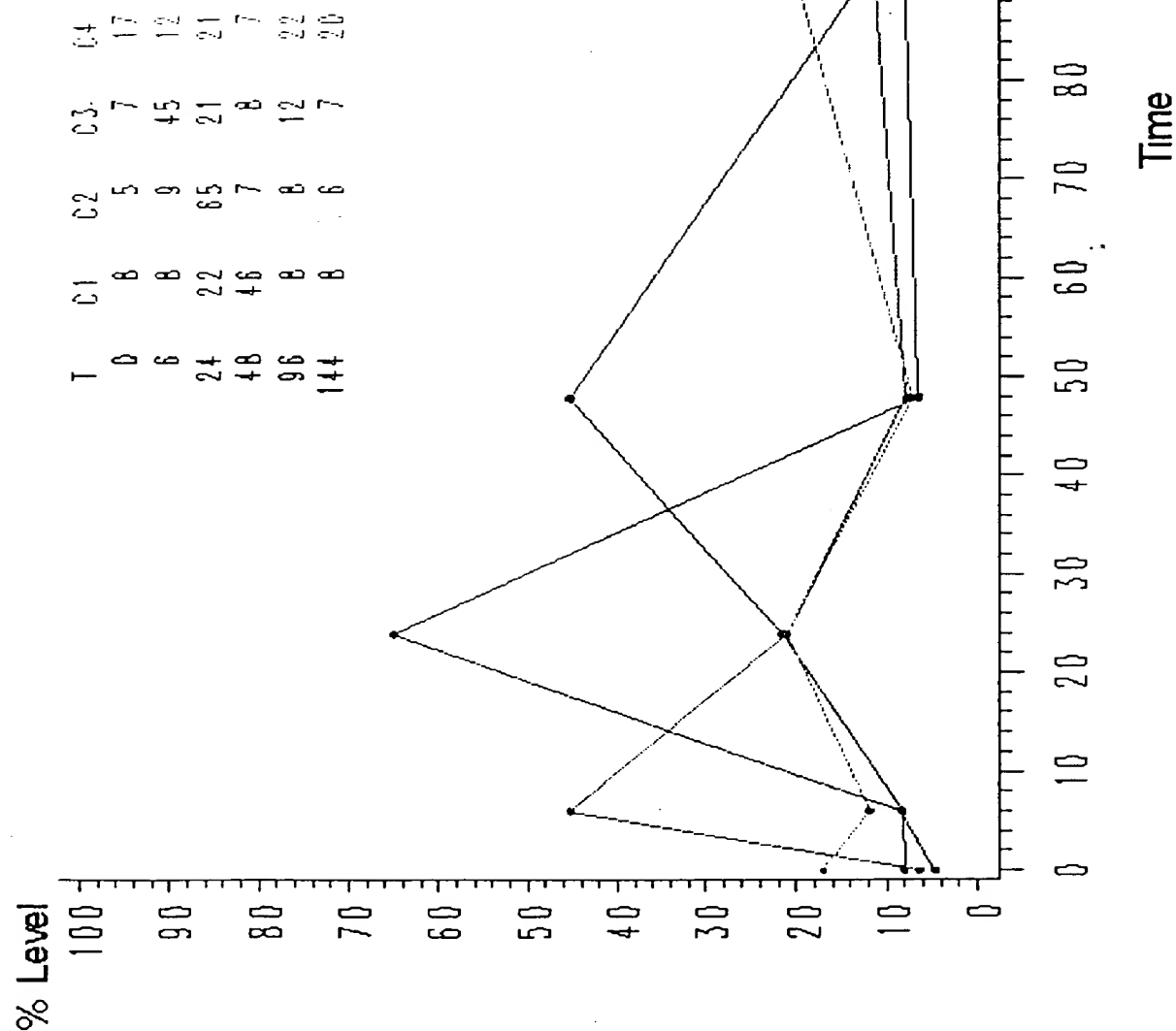


FIGURE 1

FIGURE 2

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ATGGGCGACAAGATCTGGCTGCCCTTCCCGTGCTCCTTCTGGCCGCTCTGCCTCCGGTGCTGCTGCCTGGGGCGGCCGG
CTTCACACCTTCCCTCGATAGCGACTTCACCTTTACCCTTCCCGCCGGCCAGAAGGAGTGCTTCTACCAGCCCATGCCCC
TGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTATAGTGGAGCAGGATTAGATATTGATTTCCATCTTGCCCTCTCCAGAA
GGCAAAACCTTAGTTTTTGAACAAAGAAAATCAGATGGAGTTCACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTG
CTTTGACAATACATTACGACCACTTTCTGAGAAGGTGATTTCTTTGAATTAATCCTGGATAATATGGGAGAACAGGCAC
AAGAACAAGAAGATTGGAAGAAATATATTACTGGCACAGATATATTGGATATGAACTGGAAGACATCCTGGAATCCATC
AACAGCATCAAGTCCAGACTAAGCAAAAGTGGGCACATACAACTCTGCTTAGAGCATTTGAAGCTCGTGATCGAAACAT
ACAAGAAAGCAACTTTGATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTCTATGGTGGTGGTGTGAGCCATTCAAG
TTTATATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAACTTAA

FIGURE 3

FIGURE 4

MGDKIWLPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFPLPAGQKECFYQPMPLKASLEIEYQVLDGAGL
DIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCFDNTFSTISEKVIFFELIDNMGEQAQEDEDWK
KYITGTDILDMKLEDILESINSIKSRLSKSGHIQTLLRAFEARDRNIQESNFDRVNFWSMVNLVVMVVVS
ATQVYMLKSLFEDKRKSRT.

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FIGURE 5

Peptide Name: AAA4p1

Sequence: H-Cys-Met-Leu-Lys-Ser-Leu-Phe-Glu-Asp-Lys
-Arg-Lys-Ser-Arg-Thr-OH

Peptide Name: AAA4p2

Sequence: H-Cys-Ala-Gly-Phe-Thr-Pro-Ser-Leu-Asp-Ser-Asp
-Phe-Thr-Phe-Thr-NH₂

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FIGURE 6

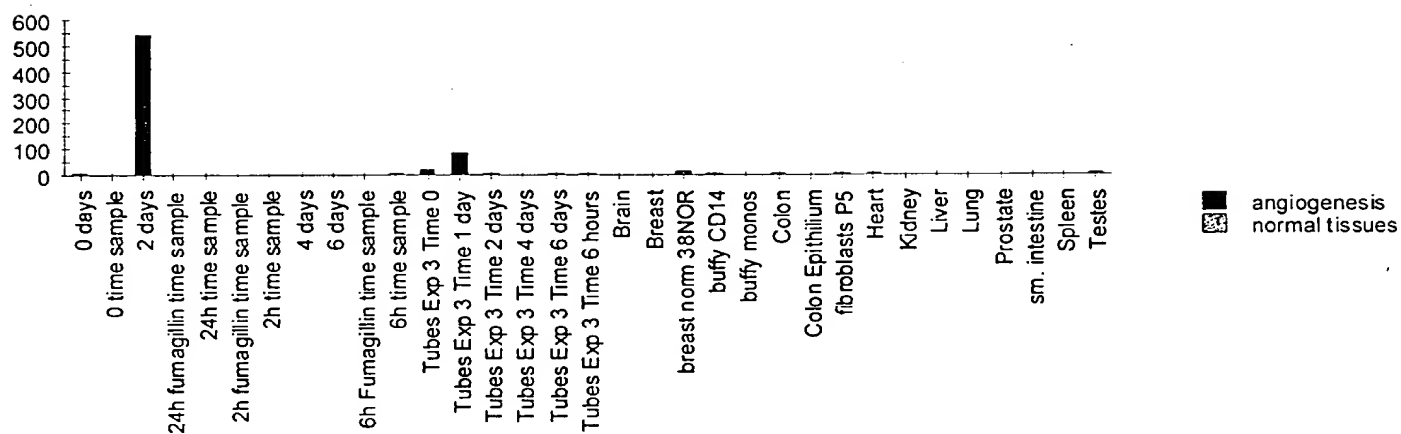


FIGURE 7

TAAAAATCGAGCTGAGATGATAGATTTCAATATCCGGATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTG
AAGTTAGTGCCCATCTGAGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGACAAAGAAGGGAATCCAGC
TCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGTAGAAAATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCAT
ACACAATGAATACAAAACCTGGAAGTCTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCC
CGCAATTCTGTTGGATATCGCAGGTGTCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCATCATAGCAGC
CGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAG
AAACCTCCTTCCAGAAGAGTAATTCTTCATCTAAAGCCACGACAATGAGTGAAAATGATTTCAAGCACACAAAATCCTTT
ATAATTTAAAGACTCCACTTTAGAGATACACCAAAGCCACCGTTGTTACACAAGTTATTAACTATTATAAACTCTGCT
TTGTCCGACATTTGCAAAGAGGTACACGAGGAAATGGAATTGGTATTTCAATTTTAAATTTTCACTACTAACTCACCTG
AACTTGCTATTTTAAACAAATAGTTCTGTCGACACCTAAAATATAATCTGGCTTCTTGTGCTCTGGACTAAGTTAAAAGAA
TTAAAATACTTTGTAATGTCAAAA

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KNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPA
PEYTWFKDGI RLLNPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN SVGYRRCPGKRMQVDDLNI SG IIAA
VVVVALVISVCGL GVCYAQRKGYFSKETS FQKSNSSSKATTMS ENDFKHTKSFI I .

FIGURE 8

FIGURE 9

Peptide Name: AAA1p1

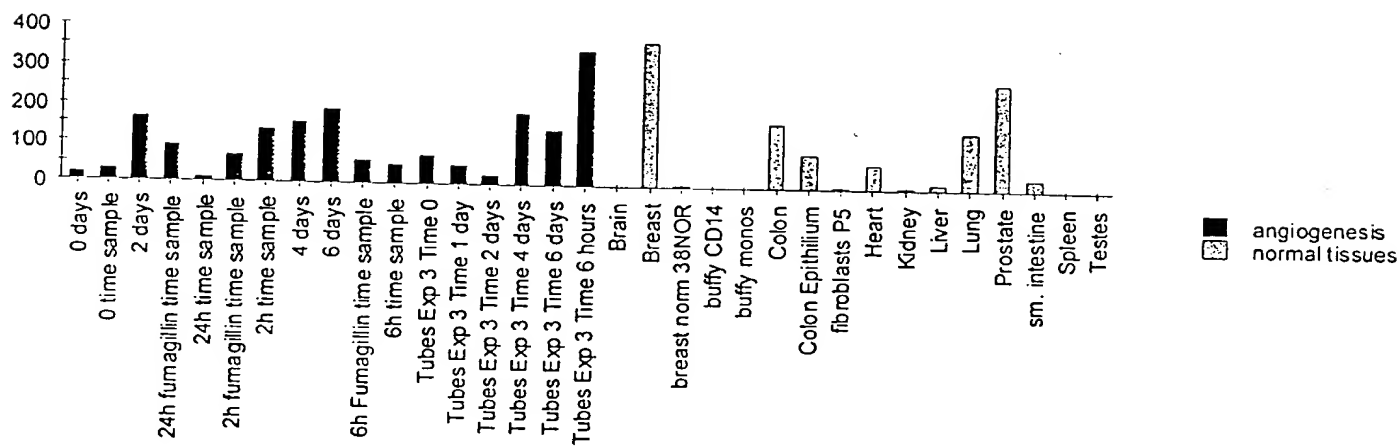
Sequence: H-Cys-Ala-Thr-Thr-Met-Ser-Glu-Asn-Asp-Phe-Lys
-His-Thr-Lys-Ser-NH₂

Peptide Name: AAA1p2

Sequence: Ac-Arg-Cys-Gln-Asp-Lys-Glu-Gly-Asn-Pro-Ala-Pro
-Glu-Tyr-Thr-NH₂

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FIGURE 10



TCTAAAGGTCGGGGGEAGGAGCAAGATGCGAAGCGAGCCGTACAGATCCCGGGCTCTCCG
AACGCAACTTCGCCCTGCTTGAGCGAGGCTGCGGTTTCCGAGGCCCTCTCCAGCCAAGGA
AAAGCTACACAAAAGCCTGGATCACTCATCGAACCACCCCTGAAGCCAGTGAAGGCTCT
CTCGCCTCGCCCTCTAGCGTTCTGTCTGGAGTAGCGCCACCCCGGCTTCCTGGGGACACAG
GGTTGGCACCATGGGGCCCACCAGCGTCCCGCTGGTCAAGGCCACCGCAGCTCGGTCTC
TGACTACGTCAACTATGATATCATCGTCCGGCATTACAACACACGGGAAAGCTGAATAT
CAGCGCGGACAAGGAGAACAGCATTAAACTGACCTCGGTGGTGTTCATTCTCATCTGCTG
CTTTATCATCTCTGGAGAACATCTTTGTCTTGCTGACCATTGGAAAACCAAGAAATTCCA
CCGACCCATGTACTATTTTATTGGCAATCTGGCCCTCTCAGACCTGTTGGCAGGAGTAGC
CTACACAGCTAACCTGCTCTTGTCTGGGGCCACCACCTACAAGCTCACTCCCGCCAGTG
GTTTCTGCGGGAAGGGAGTATGTTTGTGGCCCTGTGAGCCTCCGTGTTTCACTCTCCTCGC
CATCGCCATTGAGCGCTATATCACAATGCTGAAAATGAAACTCCACAACGGGAGCAATAA
CTTCCGCCTCTTCTGCTAATCAGCGCCTGCTGGGTCTCTCCCTCATCTGCGGTGGCCT
GCCTATCATGGGCTGGAAGTGCATCAGTGCCTGTCCAGCTGCTCCACCGTGTGCGGCT
CTACCACAAGCACTATATCTCTTCTGCACCACGGTCTTCACTCTGCTTCTGCTCTCCAT
CGTCATTCTGTACTGCAGAATCTACTCCTTGGTCAGGACTCGGAGCCGCCCTGACGTT
CCGCAAGAACATTTCCAAGGCCAGCCGAGCTCTGAGAATGTGGCGCTGCTCAAGACCGT
AATTATCGTCCTGAGCGTCTTTCATCGCCTGCTGGGCACCGCTCTTCATCTGCTCTGCT
GGATGTGGGCTGCAAGGTGAAGACCTGTGACATCCTCTTTCAGAGCGGAGTACTTCTGGT
GTTAGCTGTGCTCAACTCCGGCACCAACCCCATCTTTTACACTCTGACCAACAAGGAGAT
GCGTCGGGCCCTTCATCCGGATCATGTCTGCTGCAAGTGCCCGAGCGGAGACTCTGCTGG
CAAATTCAGCGACCCATCATCGCCGGCATGGAATTCAGCCGAGCAAATCGGACAATTC
CTCCCACCCCGAGAAAGACGAAGGGGACAACCCAGAGACCATTATGTCTTCTGGAACGT
CAACTCTTCTTCTAGAACTGGAAGCTGTCCACCCACCGGAAGCGCTCTTTACTTGGTCTG
CTGGCCACCCAGTGTTTGGAAAAAATCTCTGGGCTTCGACTGCTGCCAGGGAGGAGCT
GCTGCAAGCCAGAGGAGGAAGGGGAGAATACGAACAGCCTGGTGGTGTGCGGTGTTGG
TGGGTAGAGTTAGTTCTGTGAACAATGCACTGGGAAGGGTGGAGATCAGGTCCCGGCCCT
GGAATATATATTCTACCCCCCTGGAGCTTTGATTTTGCAGTGAAGGCTAGCATT
GTCAAGCTCCTAAAGGGTTCAATTTGGCCCCCTCCTCAAAGACTAATGTCCCATGTGAAAG
CGTCTCTTTGTCTGGAGCTTTGAGGAGATGTTTTCCTTCACTTTAGTTTCAAACCCAAAGT
GAGTGTGTGCACTTCTGCTTCTTTAGGGATGCCCTGTACATCCCACACCCACCCCTCCCT
TCCCTTCATACCCCTCCTCAACGTTCTTTTACTTTATACTTTAACTACCTGAGAGTTATC
AGAGCTGGGGTTGTGGAATGATCGATCATCTATAGCAAATAGGCTATGTTGAGTACGTAG
GCTGTGGGAAGATGAAGATGGTTTGGAGGTGTAAACAATGTCTTCGCTGAGGCCAAAG
TTTCCATGTAAAGCGGGATCCGTTTTTGGAAATTTGGTTGAAGTCACTTTGATTTCTTTAA
AAAACATCTTTTCAATGAAATGTGTTACCATTTTCATATCCATTGAAGCCGAAATCTGCAT
AAGGAAGCCCACTTTATCTAAATGATATTAGCCAGGATCCTTGGTGTCTTAGGAGAAACA
GACAAGCAAAACAAAGTGAAAACCGAATGGATTAACTTTTGCAAACCAAGGGAGATTTCT
TAGCAAATGAGTCTAACAAATATGACATCCGTCTTTCCCACTTTGTTGATGTTTATTTT
AGAATCTTGTGTGATTCAATTTCAAGCAACAACATGTTGTATTTGTTGTGTTAAAGTAC
TTTTCTTGATTTTTGAATGTATTTGTTTCAGGAAGAAGTCATTTTATGGATTTTCTAAC
CCGTGTTAACTTTTCTAGAATCCACCCCTCTTGTGCCCTTAAGCATTACTTTAACTGGTAG
GGAACGCCAGAACTTTTAAGTCCAGCTATTCATTAGATAGTAATTGAAGATATGTATAAA
TATTACAAAGAATAAAAAATATATTACTGTCTCTTTAGTATGGTTTTTCAGTGCAATTAAAC
CGAGAGATGTCTTGTTTTTTTTAAAAAGAATAGTATTTAATAGGTTTCTGACTTTTGTGGA
TCATTTTGCACATAGCTTTATCAACTTTTAAACATTAATAAACTGATTTTTTTTAAAG

FIGURE 11

FIGURE 12

ATGGGGCCCCACCAGCGTCCCGCTGGTCAAGGCCCCACCGCAGCTCGGTCTCTGACTACGTCAACTATGATATCATCGTCCG
GCATTACAACCTACACGGGAAAGCTGAATATCAGCGCGGACAAGGAGAACAGCATTAAACTGACCTCGGTGGTGTTTCATTC
TCATCTGCTGCTTTATCATCCTGGAGAACATCTTTGTCTTGCTGACCATTGGAACCAAGAAATTCCACCGACCCATG
TACTATTTTATTGGCAATCTGGCCCTCTCAGACCTGTTGGCAGGAGTAGCCTACACAGCTAACCTGCTCTTGTCTGGGGC
CACCACCTACAAGCTCACTCCCGCCAGTGGTTTCTGCGGGAAGGGAGTATGTTTGTGGCCCTGTCAGCCTCCGTGTTCA
GTCTCCTCGCCATCGCCATTGAGCGCTATATCACAATGCTGAAAATGAACTCCACAACGGGAGCAATAACTTCCGCCTC
TTCCTGCTAATCAGCGCCTGCTGGGTCATCTCCCTCATCCTGGGTGGCCTGCCTATCATGGGCTGGAAGTGCATCAGTGC
GCTGTCCAGCTGCTCCACCGTCTGCCGCTCTACCACAAGCACTATATCCTCTTCTGCACCACGGTCTTCACTCTGCTTC
TGCTCTCCATCGTCATTCTGTACTGCAGAATCTACTCCTTGGTCAGGACTCGGAGCCGCCGCTGACGTTCCGCAAGAAC
ATTTCCAAGGCCAGCCGAGCTCTGAGAATGTGGCGCTGCTCAAGACCGTAATTATCGTCCTGAGCGTCTTCATCGCCTG
CTGGGCACCGCTCTTCATCCTGCTCCTGCTGGATGTGGGCTGCAAGGTGAAGACCTGTGACATCCTCTTCAGAGCGGAGT
ACTTCCTGGTGTTAGCTGTGCTCAACTCCGGCACCAACCCCATCATTTACACTCTGACCAACAAGGAGATGCGTCGGGCC
TTCATCCGGATCATGTCCTGCTGCAAGTGCCCGAGCGGAGACTCTGCTGGCAAATTCAAGCGACCCATCATCGCCGGCAT
GGAATTCAGCCGAGCAAATCGGACAATTCCTCCACCCCCAGAAAGACGAAGGGGACAACCCAGAGACCATTATGTCTT
CTGGAAACGTCAACTCTTCTTCCTAG

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FIGURE 13

MGPTSVPLVKAHRSSVSDYVNYDIIVRHYNITGKLNISADKENSIKLTSVVFILICCFIILENIFVLLTIWKTCKFHRPM
YYFIGNLALSDLLAGVAYTANLLLSGATTYKLTPAQWFLREGSMFVALSASVFSLLAIAIERYITMLKMKLHNGSNNFRI
FLLISACWVISLILGGLPIMGWNCISALSSCSTVLPYHKHYILECTTVFTLLLLSIVILYCRYSLVRTRSRLTFRKN
ISKASRSSENVALLKTVIIVLSVFIACWAPLFIILLLDVGCKVKTCDILFRAEYFLVLAVLNSGTNPIIYTLTNKEMRRA
FIRIMSCCKCPSGDSAGKFKRPIIAGMEFSRSKSDNSSHPQKDEGDNPETIMSSGNVNSSS.

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FIGURE 14

Peptide names	amino acid sequence	Solubility
AAA7p1	Ac-KLNISADKENS IKLC-NH2	1mg/1ml H2O
AAA7p2	H-CTTYKLTPAQWFLRE-NH2	min.amt.DMSO/H2O
AAA7p3	H-CNP I IYTLTNKEMRR-NH2	1mg/1ml H2O
AAA7p1m	Ac-KLNIGA EKDHGIKLC-NH2	1mg/1ml H2O

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FIGURE 15

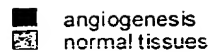


FIGURE 16

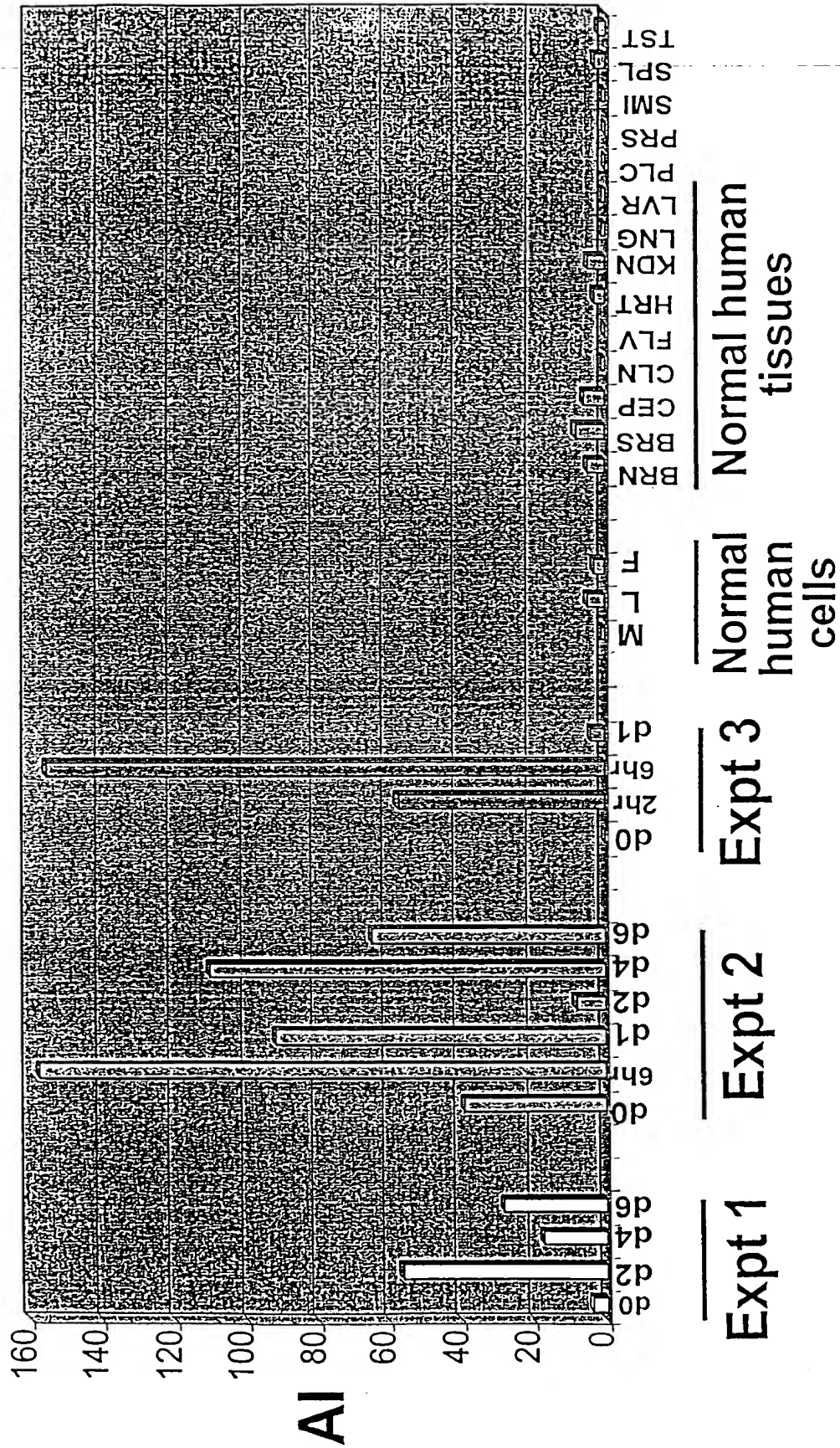


FIGURE 17

CAGGACAGGGAAGAGCGGGCGCTATGGGGAGCCGGACGCCAGAGTCCCCTCTCCACGCCGTGCAGCTGCG
CTGGGGCCCCCGGCGCCGACCCCEGCTCGTGCCGCTGCTGTTGCTGCTCGTGCCGCCGCCACCCAGGGTC
GGGGGCTTCAACTTAGACGCGGAGGCCCCAGCAGTACTCTCGGGGCCCCGGGCTCCTTCTCGGATTCT
CAGTGGAGTTTTACCGGCCGGGACAGACGGGGTCAGTGTGCTGGTGGGAGCACCCAGGCTAATACCAG
CCAGCCAGGAGTGTGCAGGGTGGTGTCTACCTCTGTCTTGGGGTGCCAGCCCCACACAGTGCACC
CCCATTGAATTTGACAGCAAAGGCTCTCGGCTCCTGGAGTCTCACTGTCCAGCTCAGAGGGAGAGGAGC
CTGTGGAGTACAAGTCCCTTGCAGTGGTTCGGGGCAACAGTTCGAGCCCATGGCTCCTCCATCTTGGCATG
CGCTCCACTGTACAGCTGGCGCACAGAGAAGGAGCCACTGAGCGACCCCGTGGGCACCTGCTACCTCTCC
ACAGATAACTTCAACCGAATCTGGAGTATGCACCTGCCGCTCAGATTTAGCTGGGCAGCAGGACAGG
GTTACTGCCAAGGAGGCTTCACTGCCGAGTTACCAAGACTGGCCGTGTGGTTTTAGGTGGACCAGGAAG
CTATTTCTGGCAAGGCCAGATCCTGTCTGCCACTCAGGAGCAGATTGCAGAATCTTATTACCCCGAGTAC
CTGATCAACCTGGTTCAGGGGCAGCTGCAGACTCGCCAGGCCAGTTCCATCTATGATGACAGCTACCTAG
GATACTCTGTGGCTGTGGTGAATTCAGTGGTGTGACACAGAAGACTTTGTTGCTGGTGTGCCCAAAGG
GAACCTCACTTACGGCTATGTCACCATCCTTAATGGCTCAGACATTGCATCCCTCTACAACTTCTCAGGG
GAAACAGATGGCTCCCTACTTTGGCTATGCAGTGGCCGCCACAGACGTCAATGGGGACGGGCTGGATGACT
TGCTGGTGGGGGCACCCCTGCTCATGGATCGGACCCCTGACGGGGCGGCTCAGGAGGTGGGCAGGGTCTA
CGTCTACCTGCAGCACCCAGCCGGCATAGAGCCACGCCACCCCTTACCCTCACTGGCCATGATGTGGCCATCG
GGCCGATTTGGCAGCTCCTTGACCCCCCTGGGGGACCTGGACCAAGGATGGCTACAATGATGTGGCCATCG
GGGCTCCCTTTGGTGGGGAGACCCAGCAGGGAGTAGTGTGTTGATTTCTGGGGGCCAGGAGGGCTGGG
CTCTAAGCCTTCCCAGGTTCTGCAGCCCTGTGGGCAGCCAGCCACACCCAGACTTCTTTGGCTCTGCC
CTTCGAGGAGGCCGAGACCTGGATGGCAATGGATACTCTGATCTGATTGTGGGGTCTTTGGTGTGGACA
AGCCTGTGGTATACAGGGGCGCCCATCGTGTCCGCTAGTGCCTCCCTCACCATCTTCCCCGCCATGTT
CAACCCAGAGGAGCGGAGCTGCAGCTTAGAGGGGAACCTGTGGCCTGCATCAACCTTAGCTTCTGCCTC
AATGCTTCTGGAAAACACGTTGCTGACTCCATTGGTTTACAGTGGAACTTCAGCTGGACTGGCAGAAGC
AGAAGGGAGGGGTACGGCGGGCACGTGTTCCCTGGCCTCCAGGCAGGCCAACCTGACCCAGACCTTGCTCAT
CCAGAATGGGGTTCGAGAGGATTCAGAGAGATGAAGATCTACCTCAGGAACGAGTCAAGATTTTCGAGAC
AACTCTCGCCGATTACATCGCTCTCACTTCTCCTTGGACCCCCAAGCCCCAGTGGACAGCCACGGCC
TCAGGCCAGCCCTACATTATCAGAGCAAGAGCCGATAGAGGACAAGGCTCAGATCTTGTGGACTGTGG
AGAAGACAACATCTGTGTGCTGACCTGCAGCTGGAAGTGTGTTGGGGAGCAGAACCATGTGTACCTGGGT
GACAAGAATGCCCTGAACTCACTTTCCATGCCCAGAATGTGGGTGAGGGTGGCGCCTATGAGGCTGAGC
TTCGGGTACCCGCCCTCCAGAGGCTGAGTACTCAGGACTCGTCAGACACCCAGGGAACCTTCTCCAGCCT
GAGCTGTGACTACTTTGCCGTGAACAGAGCCGCTGCTGGTGTGTGACCTGGGCAACCCCATGAAGGCA
GGAGCCAGTCTGTGGGTGGCCTTCGGTTTACAGTCCCTCATCTCCGGGACACTAAGAAAACCATCCAGT
TTGACTTCCAGATCCTCAGCAAGATCTCAACAACTCGCAAGCCTGAGGCAGTGCTATTCCCAGTAAGCGAC
GGAGCCTCAGGCCAGGTCACCTGAACGGTGTCTCCAAGCCTGAGGCAGTGCTATTCCCAGTAAGCGAC
TGGCATCCCCGAGACCAGCCTCAGAAAGGAGGAGCCTGGGACCTGCTGTCCACCATGTCTATGAGCTCA
TCAACCAAGCCCCAGCTCCATTAGCCAGGGTGTGCTGGAACCTCAGCTGTCCCCAGGCTCTGGAAGGTCA
GCAGCTCCTATATGTGACCAGAGTTACGGGACTCACTGCACCACCAATACCCCATTAACCCAAAGGGC
CTGGAGTTGGATCCCGAGGGTTCCCTGCACCACCAGCAAAAACGGGAAGCTCCAAGCCGAGCTCTGCTT
CCTCGGGACCTCAGATCCTGAAATGCCCGGAGGCTGAGTGTTCAGGCTGCGCTGTGAGCTCGGGCCCCCT
GCACCAACAAGAGAGCCAAAGTCTGCAGTTGCATTTCCGAGTCTGGGCCAAGACTTTCTTGACGCGGGAG
CACCAGCCATTTAGCCTGCAGTGTGAGGCTGTGTACAAAGCCCTGAAGATGCCCTACCGAATCCTGCCTC
GGCAGCTGCCCCAAGAGAGCGTCAGGTGGCCACAGCTGTGCAATGGACCAAGGCAGAAAGGCAGCTATGG
CGTCCCCTGTGGATCATCATCCTAGCCATCCTGTTTGGCCTCCTGCTCCTAGGTCTACTCATCTACATC
CTCTACAAGCTTGGATCTTCAACGCTCCCTCCCATATGGCACCGCCATGGAAAAGCTCAGCTCAAGC
CTCCAGCCACCTCTGATGCCCTGAGTCTCTCCCAATTTAGACTCCCATTTCTGAAGAACCAAGTCCCCCAG
CCTCATTTCTACTGAAAAGGAGGGGTCTGGGTACTTCTTGAAGGTGCTGACGGCCAGGGAGAAGCTCCTCT
CCCCAGCCAGAGACATACTTGAAAGGGCCAGAGCCAGGGGGGTGAGGAGCTGGGGATCCCTCCCCCCCCAT
GCACTGTGAAGGACCCCTTGTTTACACATACCTCTTCAATGGATGGGGGAACCTCAGATCCAGGGACAGAGG
CCCAGCCTCCCTGAAGCCTTTGCATTTTGGAGAGTTTCTGAAACAACCTGGAAAGATAACTAGGAATCC
ATTCACAGTTCTTTGGGCCAGACATGCCACAAGGACTTCTGTCCAGCTCCAACTGCAAGATCTGTCC
TCAGCCTTGCCAGAGATCCAAAAGAAGCCCCCAGTAAAGAACCTGGAACCTGGGGAGTTAAGACCTGGCAG
CTCTGGACAGCCCCACCCCTGGTGGGCCAACAAAGCACTAATATGCATGGTGGCCCGACGACCTCA
GGACAGATGCCACAAAGGATAGATGCTGGCCAGGCCAGGCCAGCTCCAAGGGGAATCAGAACTCAA
TGGGCCAGATCCAGCCTGGCGTCTGGAGTTGATCTGGAACCCAGACTCAGACATTGGCACCALTCCAGG
CAGATCCAGGACTATATTTGGGCCTGCTCCAGACCTGATCCTGGAGGCCAGTTACCCCTGATTTAGGAG
AAGCCAGGAATTTCCCAGGACCTGAAGGGGGCATGATGGCAACAGATCTGGAACCTCAGCCTGGCCAGAC
ACAGGCCCTCCCTGTTCCCCAGAGAAAGGGGAGCCCACTGTCTGGGCCTGCAGAATTTGGGTCTGTGCT
GCCAGCTGCATGATGCTGCCCTCATCTCTGCCCCAACCTTCCCTCACCTTGGCACCAGACACCCAG
GACTTATTTAACTCTGTGCAAGTGCAATAAATCTGACCCAGTGCCCCCACTGACCAGAACTAGAAAAA
AAAA

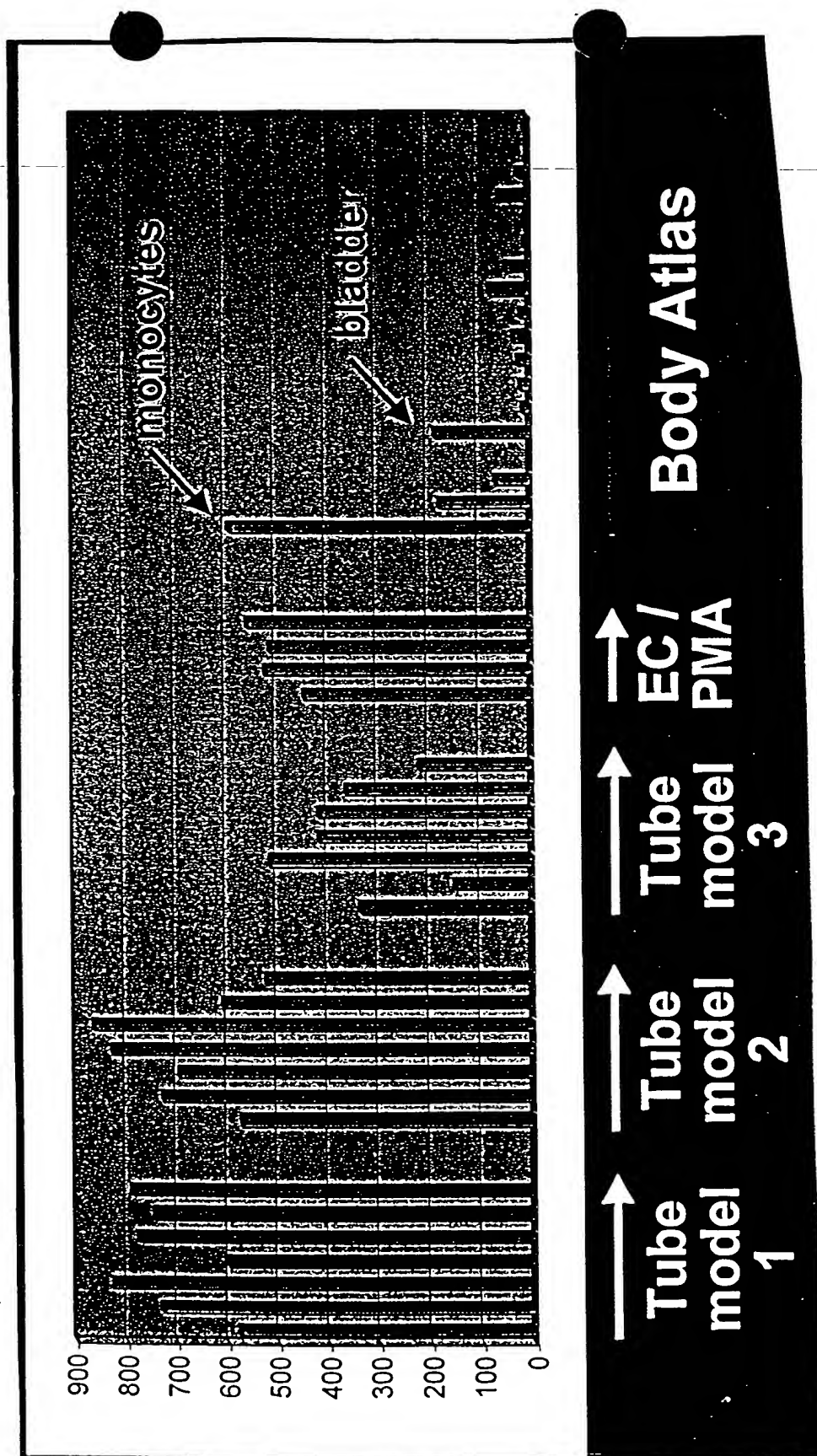
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FIGURE 18

MGSRT¹PESPLHAVQLRWGPRRRPPLVPLLLLLLVPPFPRVGGFNLD²AEPAVL³SGPPGSFFGFSVEFYRPGTDGVS⁴VLVGA
FKANTSQPGVLQGGAVYLCPWGASPTQCTPIEFDSKGSRLLESSLSSEGE⁵EPVEYKSLQWFGATVRANGSSILACAPLY
SWRTEKEPLSDPVGTCYLSTDN⁶FTRILEYAPCRSDFSWAAGQGYCQGGFSAEFTKTGRVVLGGPGSYFWQGQILSATQEQ
IAESYYPEYLINLVQGGQLQTRQASSIYDDSYLGYSVAVGEFSGDDTEDFVAGVPKGNLTYGYVTILNGSDIRSLYNFSGE
QMASYFGYAVAATDVNGDGLD⁷LLVGAPILMDRTPDGRPQEVGRVYVYLQHPAGIEPTPTLTLTGHDEFGRFGSSITPIG
DLDQOGYNDVAIGAPFGGETQQGVVFVFPGGPGGLGSKPSQVLQPLWAASHTPDFFGSALRGGRDLGNGYPDLIVGSFG
VDKAVVYRGRPIVSASASLTIFPAMFNPEERSCSLEGNPVACINLSFC⁸LNASGKHVADSIGFTVELQLDWQKQKGGVRRN
LFLASRQATLTQTLLIQNGAREDCREMKIYLRNESEFRDKLSPIHIALNFS⁹LDPQAPVD¹⁰SHGLRPALHYQSKSRIEDKAQ
ILI.DCGEDNICVPDLQLEVFGEQNHVYLGDKNALNLTFHAQNVGEGGAYE¹¹AE¹²LRVTAPPEAEYSGLVRHFGNFS¹³SLSCDY
FAVNQSRI.LVCDLGNPMKAGASLWGGLRFTVPHLRDTKKTIQFDFQILSKNLNNSQSDVVSFRLSVEAQAQVTLNGVSKP
EAVLF¹⁴PVSDWHPRDQ¹⁵QKEEDLGPVHHVYELINQGPSSISQGVLELSC¹⁶PQALEGQQLLYVTRVTGINCTTNHPIN¹⁷PKGL
ELDPEGSLHHQKRFAPSRSSASSGFQILKCEAECFRLRCELGPLHQ¹⁸QESQSLQLHFRVWAKTFLQREHQPFSLQCEAV
YKALKMPYRILPRQLPQKERQVATAVQWTKAEGSYGVPLWIIILAILEGLLLLGLLIYI¹⁹LYKLGF²⁰FKRSLPYGTAMEKAQ
LKPFATSDA

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FIGURE 19



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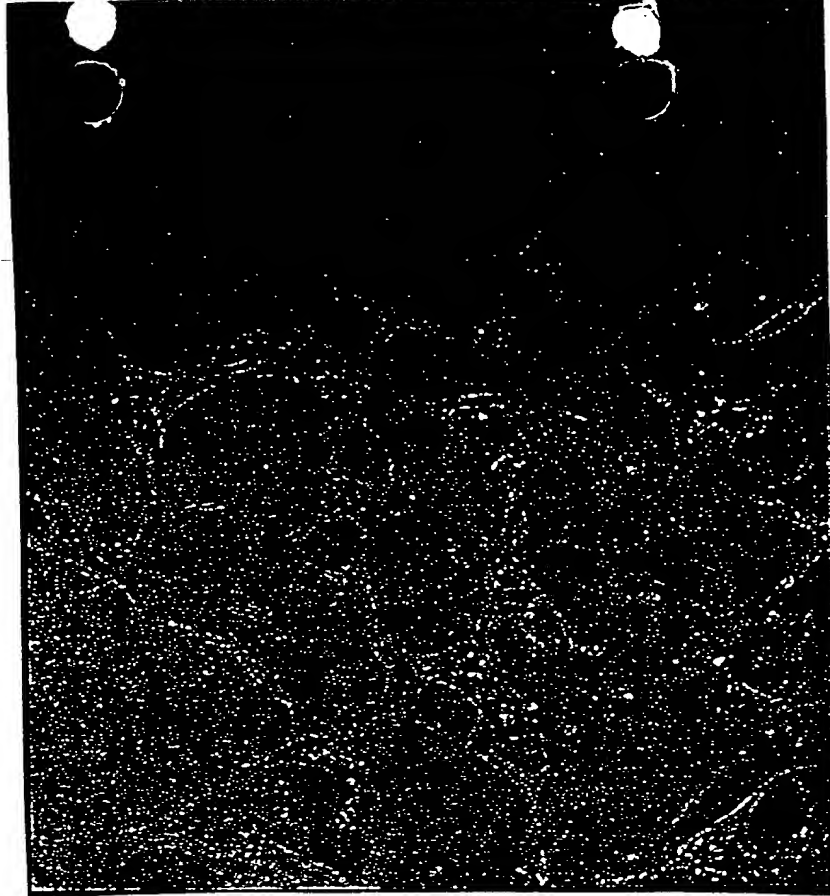
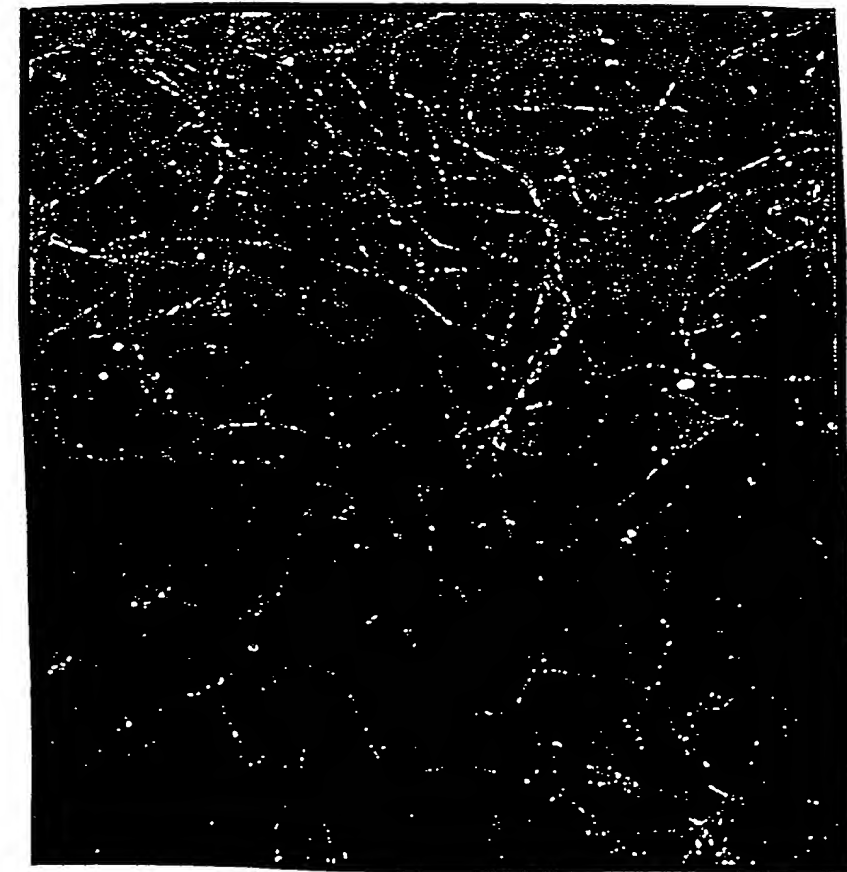


FIGURE 20

AAA9 cDNA Sequence

AAGGCCCTGCCAGCTTGGGAGGGAATTGTCCCTGCCTGCTTCTGGAGAAAGAAGATATTGACACCATCTAC
GGGCACCATTGAAGTGCCTTCAAGTGACCATTCCTTTTCTTCTGCCCAGTATTTGCAGCAGTAACAGCACAG
GTGTTTTAGAGGCAGCTAATAATTCAGTGTGTTACTACAACAAAACCATCTATAACAACACCAACACA
GAATCATTACAGAAAAATGTTGTCAACCAACAACCTGGAACAACCTCCTAAAGGAACAATCACCAATGAATT
ACTTAAATGTCTCTGATGTCAACAGCTACTTTTTTAACAAGTAAAGATGAAGGATTGAAAGCCACAACCA
CTGATGTCAGGAAGAATGACTCCATCATTTCAAACGTAACAGTAACAAGTGTTACACTTCCCAATGCTGTT
TCAACATTACAAAGTTCCAAACCCAAGACTGAAACTCAGAGTTCAATTAAAAACAACAGAAATACCAGGTAG
TGTTCTACAACCAGATGCATCACCTTCTAAACTGGTACATTAACCTCAATACCAGTTACAATTCCAGAAA
ACACCTCACAGTCTCAAGTAATAGRCAGTGAAGGTGGAAAAAATGCAAGCACTTCAGCAACCAGCCGGTCT
TATTCCAGTATTATTTTGGCGGTGGTTATTGCTTTGATTGTAATAACACTTTCAGTATTTGTTCTGGTGGG
TTTGTACCGAATGTGCTGGAAGGCAGATCCGGGCACACCAGAAAATGGAAATGATCAACCTCAGTCTGATA
AAGAGAGCGTGAAGCTTCTTACCGTTAAGACAATTTCTCATGAGTCTGGTGAGCACTCTGCACAAGGAAAA
ACCAAGAACCTCAGCTTGAGGAATTCTCTCCACACCTAGGCAATAATTACGCTTAATCTTCAGCTTCTAT
GCACCAAGCGTGGAAGGAGAAAGTCTGCAGAATCAATCCCGACTTCCATACCTGCTGCTGGACTGTAC
CAGACGTCTGTCCAGTAAAGTGATGTCCAGCTGACATGCAATAATTTGATGGAATCAAAAAGAACCCCGG
GGCTCTCCTGTTCTCTCACATTTAAAAATTCCATTACTCCATTTACAGGAGCGTTCCTAGGAAAAGGAATT
TTAGGAGGAGAATTTGTGAGCAGTGAATCTGACAGCCCAGGAGGTGGGCTCGCTGATAGGCATGACTTTCC
TTAATGTTTTAAAGTTTTCCGGGCCAAGAATTTTTATCCATGAAGACTTTCCTACTTTTCTCGGTGTTCTTA
TATTACCTACTGTTAGTATTTATTGTTTACCACATATGTTAATGCAGGGAAAAGTTGCACGTGTATTATTAA
ATATTAGGTAGAAATCATACCATGCTACTTTGTACATATAAGTATTTTATTCCTGCTTTCGTGTTACTTTT
AATAAATACTACTGTACTCAATACTCTAAAAATACTATAACATGACTGTGAAAATGGCAATGTTATTGTC
TTCCTATAATTATGAATATTTTGGATGGATTATTAGAATACATGAACTCACTAATGAAAGGCATTTGTAA
TAAGTCAGAAAGGGACATAGGATTACATATCAGACTGTTAGGGGGAGAGNTAATTATCAGTTCCTTGGTC
TTTCTATTTGTCATTCTACTATGTGATGAAGATGTAAGTGCAAGGGCATTATATAACACTATACTGCATT
ATTAGATAT

FIGURE 21

AAA9 Protein

MELLOVTILELLPSICSSNSTGVLEAANNSLVVTTTKPSITTPNTESLQKNVVTPTTGTPKGTITNELLK
MSLMSTATFLTskDEGLKATTTDVRKNDISIISNVTVTSVTLPNVSTLQSSKPKTETQSSIKTTEIPGSVL
QPDASPSKTGTLTIPVTIPENTSQSQVIXTEGGKNASTSATSRSYSSIILP
RMCWKADPGTPENGNDQPQSDKESVKLLTVKTI SHESGEHSAQGKTKN

FIGURE 22

AAB4 (MMP10)

ATG CATCTTGCATTCCTTGTGCTGTTGTGTCTGCCAGTCTGCTCTGCCTATCCTCTGAGTGGGG
CAGCAAAAGAGGAGGACTCCAACAAGGATCTTGCCAGCAATACCTAGAAAAGTACTACAAC
CTCGAAAAGGATGTGAAACAGTTTAGAAGAAAGGACAGTAATCTCATTGTTAAAAAAATCCA
AGGAATGCAGAAGTTCCTTGGGTGGAGGTGACAGGGAAGCTAGACACTGACACTCTGGAGG
TGATGCGCAAGCCCAGGTGTGGAGTTCCTGACGTTGGTCACTTCAGCTCCTTTCTGGCATGCC
GAAGTGGAGGAAAACCCACCTTACATACAGGATTGTGAATTATACACCAGATTTGCCAAGAG
ATGCTGTTGATTCTGCCATTGAGAAAAGCTCTGAAAGTCTGGGAAGAGGTGACTCCACTCACAT
TCTCCAGGCTGTATGAAGGAGAGGCTGATATAATGATCTCTTTCGCAGTTAAAGAACATGGAG
ACTTTTACTCTTTTGATGGCCAGGACACAGTTTGGCTCATGCCTACCCACCTGGACCTGGGCT
TTATGGAGATATTCATTTTGATGATGATGAAAAATGGACAGAAGATGCATCAGGCACCAATTT
ATTCCTCGTTGCTGCTCATGAACTTGGCCACTCCCTGGGGCTCTTTCACTCAGCCAACACTGAA
GCTTTGATGTACCCACTCTACAACCTCATTACAGAGCTCGCCAGTTCCGCCTTTTCGCAAGATG
ATGTGAATGGCATTCACTCTCTACGGACCTCCCTGCCTCTACTGAGGAACCCCTGGTGCC
CACAAAATCTGTTCTTCGGGATCTGAGATGCCAGCCAAGTGTGATCCTGCTTTGTCCTTCGAT
GCCATCAGCACTCTGAGGGGAGAATATCTGTTCTTTAAAGACAGATATTTTGGCGAAGATCC
CACTGGAACCCCTGAACCTGAATTTCAATTTGATTTCTGCATTTTGGCCCTCTCTTCCATCATATTT
GGATGCTGCATATGAAGTTAACAGCAGGGACACCGTTTTTATTTTAAAGGAAATGAGTTCTG
GGCCATCAGAGGAAATGAGGTACAAGCAGGTTATCCAAGAGGCATCCATACCCCTGGGTTTTTC
CTCCAACCATAAGGAAAATTGATGCAGCTGTTTCTGACAAGGAAAAGAAGAAAACATACTTC
TTTGCAGCGGACAAATACTGGAGATTTGATGAAAATAGCCAGTCCATGGAGCAAGGCTTCCCT
AGACTAATAGCTGATGACTTTCCAGGAGTTGAGCCTAAGGTTGATGCTGTATTACAGGCATTT
GGATTTTCTACTTCTTCAGTGGATCATCACAGTTTGAGTTTGACCCCAATGCCAGGATGGTGA
CACACATATTAAGAGTAACAGCTGGTTACATTGCTCTAGA **TAG**

FIGURE 23

AAB4

X07820

Go

Find/Filter

Full Length Cloning

Expression

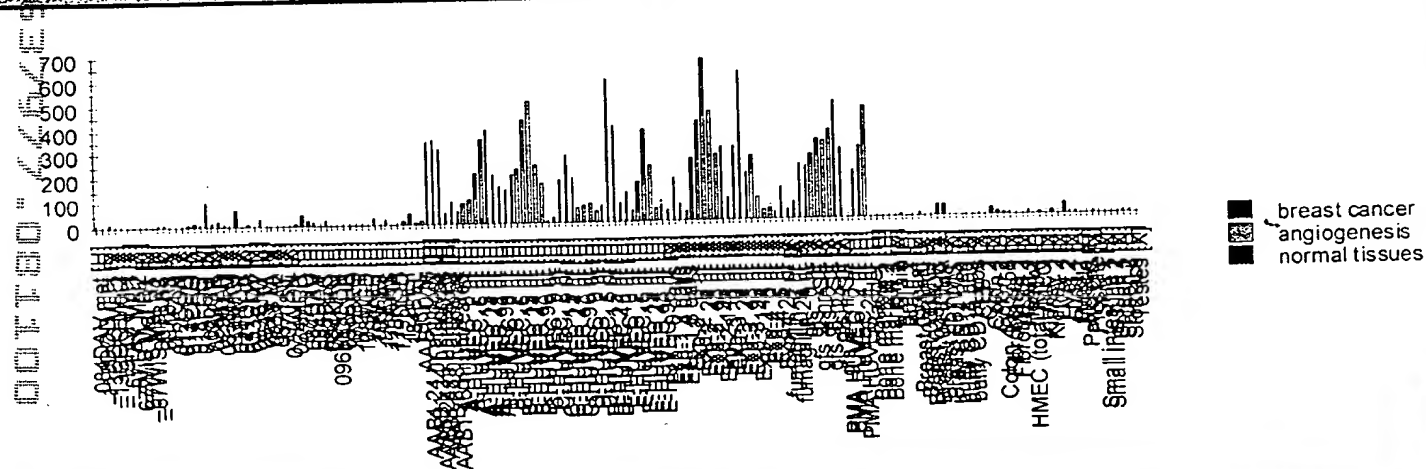
Peptides/Antibodies

Patent Info

Reports

Matrix Metalloproteinase 10 (Stromolysin 2)

UniGene ID	Hs.2258	Species	Human	Chromosome	11
5' chip PROBESET	A_RC_AA234743	sequence		Cytoband	
chip set primary key	9999999	Sequencer file	Aab4.spf	GB4 R1 bp000	352.42
RT chip primary key	102915	orthologs	Mouse, Rat	associated with CGH	
Pangea Contig	cluster2091_1	ortholog alignment file		subcellular localization	
contig length (bp)	1755	projects	Angio	SS? Yes	TM? No
ORF length (bp)	46	recommendations	MMP10, RT-PCR oligos due 3-6-00		
full-length?	yes	protein comments			



<input type="checkbox"/> Breast Cancer	<input type="checkbox"/> Angiogenesis	<input type="checkbox"/> Normal Tissues	<input type="checkbox"/> All Tissues	<input checked="" type="checkbox"/> Breast Cancer	<input checked="" type="checkbox"/> Angiogenesis	<input checked="" type="checkbox"/> Normal Tissues	Update graph
<input type="checkbox"/> Lung	<input type="checkbox"/> Liver	<input type="checkbox"/> Kidney	<input type="checkbox"/> Pancreas	<input type="checkbox"/> Small Intestine	<input type="checkbox"/> Colon	<input type="checkbox"/> HMEC (toxic)	Go to rev. 4 data

FIGURE 25